

APPENDIX B
MARKED-UP VERSION OF SUBSTITUTE SEQUENCE LISTING
WITH MARKINGS TO SHOW CHANGES MADE
(Application Serial No. 10/046,671)

SEQUENCE LISTING

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<120> Mosaic Infectious Bursal Disease Virus Vaccines

<130> 2183-5238US

<140> US 10/046,671
 <141> 2002-01-14

<150> PCT/NL00/00493
 <151> 2000-07-13

<150> EP 99202316.8
 <151> 1999-07-14

<160> 87

<170> PatentIn Ver. 2.1

<210> 1
 <211> 6
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: KpnI restriction site

<400> 1
 ggtaac 6

<210> 2
 <211> 16
 <212> DNA
 <213> Infectious bursal disease virus

<220> <221> misc_feature
 <223> Primer ANC1

<400> 2
 ggggacccgc gaacgg 16

<210> 3
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

<220>
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 <223> Primer RTAM

<400> 3
aattggtgtc cacacctg 18

<210> 4
<211> 18
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer RTAP

<400> 4
atacaggacc taactggg 18

<210> 5
<211> 30
<212> DNA
<213> Infectious bursal disease virus

<220>
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<223> Primer HY3P

<400> 5
aacgttttcc tcacaatccg cgggactggg 30

<210> 6
<211> 22
<212> DNA
<213> Infectious bursal disease virus

<220>
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<223> Primer AGTM

<400> 6
gagactccca ggtacctcac tc 22

<210> 7
<211> 18
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer AC3

<400> 7
ggtagccaca tgtgacag 18

<210> 8
<211> 21
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer HY3MR

<400> 8
ccagtcccgc ggattgtgag g

21

<210> 9
<211> 17
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer M13F-17

<400> 9
gtaaaacgac ggccagt

17

<210> 10
<211> 18
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer AC4

<400> 10
accagccaa tcacatcc

18

<210> 11
<211> 19
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer AC9

<400> 11
ctcaaagaag atggagacc

19

<210> 12

<211> 24
<212> DNA
<213> Infectious burşal disease virus

<220>
<221> misc_feature
<223> Primer M13F-24

<400> 12
cgccagggtt ttcccagtca cgac

24

<210> 13
<211> 22
<212> DNA
<213> Infectious bursal disease virus

<220>
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<223> Primer AC5

<400> 13
aaggccttca tggaggtggc cg

22

<210> 14
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<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer AGTP

<400> 14
cttgagtgag gtacctggga g

21

<210> 15
<211> 21
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer vvVP3CM

<400> 15
gagaaaattt cgcattccgat g

21

<210> 16
<211> 22
<212> DNA
<213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer M13R

 <400> 16
 tcacacagga aacagctatg ac 22

 <210> 17
 <211> 30
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
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 <223> Primer ATG3

 <400> 17
 catcgctgcg atcgtttgtc tgatctctac 30

 <210> 18
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <223> Primer

 <400> 18
 atccgggccc taaggagg 18

 <210> 19
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
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 <223> Primer ANC4"

 <400> 19
 gccaaagtcgg tgtgcag 17

 <210> 20
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature

<223>Primer HY0P
 <400> 20
 tatcattgat ggtcagtaga g 21
 <210> 21
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer HY2M
 <400> 21
 caccggcaca gctatcc 17
 <210> 22
 <211> 26
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer T7EcoRI
 <400> 22
 ggaattctaa tacgactcac tatagg 26
 <210> 23
 <211> 21
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer HY3M
 <400> 23
 ccagtcccgc ggattgtgag g 21
 <210> 24
 <211> 17
 <212> DNA
 <213> Infectious bursal disease virus
 <220>
 <221> misc_feature
 <223> Primer M13F
 <400> 24

gtaaaacgac ggccagt 17

<210> 25
<211> 16
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer HY4M

<400> 25
ccggcacagc tadcct 16

<210> 26
<211> 17
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer ANC2

<400> 26
ctgcctgtcc tggagcc 17

<210> 27
<211> 20
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer HY4P

<400> 27
acataatccg ggccataagg 20

<210> 28
<211> 17
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<223> Primer ANC3

<400> 28
cgatgggcgt tcgggtc 17

<210> 29
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer ANC5

<400> 29
 cccatctgga gcatatcc

18

<210> 30
 <211> 18
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <223> Primer AC6

<400> 30
 ttcacctggg gtactccg

18

<210> 31
 <211> 30
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> primer_bind
 <222> (1)..(30)
 <223> Anchor

<400> 31
 cacgaattca ctatcgattc tggatccttc

30

<210> 32
 <211> 20
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> primer_bind
 <222> (1)..(20)
 <223> Anchor primer

<400> 32
 gaaggatcca gaatcgatag

20

<210> 33
 <211> 19

<212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(19)
 <223>Primer ANC0

 <400> 33
 ggggacccgc gaacggatc 19

 <210> 34
 <211> 16
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(16)
 <223> Primer ANC1

 <400> 34
 ggggacccgc gaacgg 16

 <210> 35
 <211> 47
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(47)
 <223> Primer T7AC0

 <400> 35
 ggaattctaa tacgactcac tataggatac gatcgggtctg accccgg 47

 <210> 36
 <211> 15
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(15)
 <223> Primer BNC1

 <400> 36
 gggggccccc gcagg 15

 <210> 37

<211> 45
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> primer_bind
 <222> (1)..(45)
 <223> Primer T7BC1"

 <400> 37
 ggaattctaa tacgactcac tataggatac gatgggtctg accct 45

 <210> 38
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 38
 ugauacgauc 10

 <210> 39
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 39
 agauacgauc 10

 <210> 40
 <211> 10
 <212> RNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_RNA
 <222> (1)..(10)
 <223> 5'-Terminus of the A-segment coding strand
 of IBDV

 <400> 40

ggauacgauc

10

<210> 41
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Consensus sequence corresponding to the
5'-terminus of the A-segment coding strand of
IBDV

<400> 41
ggauacgauc

10

<210> 42
<211> 4
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(4)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 42
cggg

4

<210> 43
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 43
cggguccc

8

<210> 44
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>

<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 44
cgggucccu

9

<210> 45
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 45
cgggucccc

9

<210> 46
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 46
cggguccccc c

11

<210> 47
<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 47
cggguccccc cu

12

<210> 48

<211> 12
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(12)
<223> Complementary sequence of the 5'-terminus
of the A-segment non-coding strand of IBDV

<400> 48
cggguccccc cc

12

<210> 49
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Consensus complementary sequence of the
5'-terminus of the A-segment non-coding strand of
IBDV

<400> 49
cggguccccc

9

<210> 50
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the B-segment coding strand
of IBDV

<400> 50
ugauacgaug

10

<210> 51
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> 5'-Terminus of the B-segment coding strand
of IBDV

<400> 51
ggauacgaug 10

<210> 52
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Consensus sequence of the 5'-terminus of
the B-segment coding strand of IBDV

<400> 52
ggauacgaug 10

<210> 53
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 53
gggggcca. 78

<210> 54
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 54
gggggccu 8

<210> 55
<211> 8
<212> RNA
<213> Infectious bursal disease virus

<220>

<221> misc_RNA
<222> (1)..(8)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 55
ggggggccc

8

<210> 56
<211> 9
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(9)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 56
ggggggcccc

9

<210> 57
<211> 10
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 57
gguggccccc

10

<210> 58
<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 58
ggggggcccc c

11

<210> 59

<211> 11
<212> RNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(11)
<223> Complementary sequence of the 5'-terminus
of the B-segment non-coding strand of IBDV

<400> 59
gggggcccc g

11

<210> 60
<211> 10
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_RNA
<222> (1)..(10)
<223> Consensus complementary sequence of the
5'-terminus of the B-segment non-coding strand of
IBDV

<400> 60
gggggcccc

10

<210> 61
<211> 119
<212> PRT
<213> Infectious bursal disease virus

<220>
<221> DOMAIN
<222> (1)..(119)
<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolates D6948, rD6948, UK661
5123, 96-C6, 97-B4, 97-B5, 97-B6, Hungary, OKYM,
TKSM and HK46

<400> 61
Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1' 5 10 15
Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30
Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45
Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 62
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 96-B4

<400> 62
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 63
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 96-C4

<400> 63
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Leu Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Asn Thr Ser Val Gln Gly Leu Ala Leu
 35 40 45
 Asn Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ser Asp Asn Gly Leu Thr Thr Gly Ile Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 64
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of a IBDV isolate 96-C5

<400> 64
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Val Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr

50 55 60
 Arg Ala Val Ala Ala Tyr Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Leu Pro Phe Asn Ile Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 65
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate 97-B3

<400> 65
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 66
 <211> 119
 <212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate Zoontjes

<400> 66

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
50 55 60

Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn Leu
65 70 75 80

Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Thr Thr Gln Pro Ile
85 90 95

Thr Ser Ile Lys Leu Val Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
100 105 110

Gly Asp Gln Met Ser Trp Ser
115

<210> 67

<211> 119

<212> PRT

<213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(119)

<223> Amino acid sequence of the hypervariable
region of VP2 of IBDV isolate OKYMT

<400> 67

Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
1 5 10 15

Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
20 25 30

Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Thr Leu
35 40 45

Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Phe Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 68
 <211> 119
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate TKSMT

<400> 68
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe His Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Asp Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Thr Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 69
 <211> 119

<212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(119)
 <223> Amino acid sequence of the hypervariable
 region of VP2 of IBDV isolate HK46-NT

<400> 69
 Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly Val
 1 5 10 15
 Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser
 20 25 30
 Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile Leu
 35 40 45
 Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile Thr
 50 55 60
 Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu
 65 70 75 80
 Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro Ile
 85 90 95
 Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala
 100 105 110
 Gly Asp Gln Met Ser Trp Ser
 115

<210> 70
 <211> 3260
 <212> DNA
 <213> Infectious bursal disease virus

<220>
 <221> misc_feature
 <222> (1)..(3260)
 <223> Consensus cDNA sequence of IBDV A-segment

<400> 70
 ggatacgatc ggtctgaccc cgggggagtc acccggggac aggcygwcaa ggycttgttc 60
 caggatggaa ctctctcttc tacaaygcta tcattgatgg tyagtagaga tcagacaaac 120
 gatcgacgag atgacraacc tgcaagatca aaccacacag attgttccgt tcatacggag 180
 ccttctgatg ccaacaaccg gaccggcgtc cattccggac gacaccctrg agaagcacac 240
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ggatccgttc gcgggtcccc                                     3260

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<210> 71
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature

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<222> (1)..(3260)

<223> cDNA sequence CEF94-A of IBV A-segment

<400> 71

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ggatccgttc gcgggtcccc                                     3260

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<210> 72
<211> 3260
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(3260)
<223> cDNA sequence D6948-A of IBV A-segment

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<400> 72
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gatcgacgag atgacgaacc tgcaagatca aaccacaacg attgttccgt tcatacggag 180
ccttctgatg ccaacaaccg gaccggcgtc cattccggac gacaccctag agaagcacac 240
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<210> 73
<211> 964
<212> DNA
<213> Infectious bursal disease virus

<220>
<221> misc_feature
<222> (1)..(964)
<223> cDNA sequence TY89-A of IBV A-segment

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<400> 73
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ccagaactcg aagacgctgt gcgtgcaatg gacgtgctg caaacgtcga cccattgttc 180
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caggccggaa gcaagtcgca gagggccaag tatggcacgg ctggctacgg agtggaggct 360
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cccc 964

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```

<210> 74
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

```

```

<220>

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<221> misc_feature
 <222> (1)..(2827)
 <223> Consensus cDNA sequence of IBV B-segment

<400> 74

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caggagtact tcccwaarta ctacccaaca caycgcccka gcaaggaraa gcccaatgc 480
taccgcgcmg ayatcgcayt actcaagcag atgatyatcy tgtttctcca ggttccmgag 540
gccammgagr rcctwaarga tgargtmacc ctmytraccc aaaacatwag rgayaargcc 600
tayggragtg ggacctacat gggacargcm acymgacttg tkgcyatgaa rgaggygcc 660
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gtycagtcra cytcmgtgta cacycmaag taccagarg tyagaaccc acagaccgcc 2580
tccaaacccg ttgttgggt ccacctgccc gccaaagarg ccaccggtgt ccaggcmgt 2640
cttctcggag caggracgag cagaccaatg gggatggagg cyccaacacg gtccaagaac 2700
gccgtgaaaa tggccaaamg gcggcaacgc caaaargaga gccgccaaya gccatgatg 2760
gaaccactca agaagaggac actaaycca gaccccgat ccccggcctt cgctgcggg 2820
ggcccc 2827

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<210> 75
 <211> 2827
 <212> DNA
 <213> Infectious bursal disease virus

 <220>
 <221> misc_feature
 <222> (1)..(2827)
 <223> cDNA sequence CEF94-B of IBDV B-segment

<400> 75
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 attttcaaca gtccacaggc gcgaagcacg atctcagcag cgttcggcat aaagcctact 180
 gctggacaag acgtggaaga actcttgatc cctaaagttt ggggtgccacc tgaggatccg 240
 cttgccagcc ctatgctgact ggcaaagttc ctgagagaga acggctacaa agttytgacg 300
 ccacggtctc tgcccagaaa tgaggagtat gagaccgacc aaataactccc agacttagca 360
 tggatgacgac agatagaagg ggctgtttta aaaccactc tatctctccc tattggagat 420
 caggagtact tcccaaagta ctacccaaca catcgcccta gcaaggagaa gcccaatgag 480
 taccgcccag acatcgact actcaagcag atgatttacc tgtttctcca ggttccagag 540
 gccaacgagg gcctaaagga tgaagtaacc ctcttgaccc aaaacataag ggacaaggcc 600
 tatggaagtg ggacctacat gggacaagca actcgacttg tggccatgaa ggaggctgac 660
 actggaagaa acccaaacaa ggatcctcta aagcttgggt acacttttga gagcatcgag 720
 cagctacttg acatcacact accggtaggc ccacccggtg aggatgacaa gccctgggtg 780
 ccactcacia gagtgccgtc accgatgttg gtactgacgg gagacgtaga tggcgacttt 840
 gaggttgaag attaccttcc caaaatcaac ctcaagtcac caagtggact accatatgta 900
 ggtcgcacca aaggagagac aattggcgag atgatagcta tctcaaacca gtttctcaga 960
 gagctatcaa cactgttgaa gcaagggtgca gggacaaagg ggtcaaacia gaagaagcta 1020
 ctcagcatgt taagtgacta ttggtactta tcatgccccg ttttgtttcc aaaggctgaa 1080
 aggtacgaca aaagtacatg gctcaccaag acccggaaca tatggctcagc tccatcccca 1140
 acacacctca tgatctctat gatcacctgg cccgtgatgt ccaacagccc aaataacgtg 1200
 ttgaacattg aagggtgtcc atcactctac aaattcaacc cgttcagagg aggggtgaac 1260
 aggatcgctg agtggatatt ggccccggaa gaaccaagg ctcttgata tgcggacaac 1320
 atatacattg tycactcaaa cacgtggtac tcaattgacc tagagaaggg tgaggcaaac 1380
 tgcactcgcc aacacatgca agccgcaatg tactacatac tcaccagagg gtggtcagac 1440
 aacggcgacc caatgttcaa tcaaacatgg gccacctttg ccatgaacat tgcccctgct 1500
 ctagtggtag actcatcgtg cctgataatg aacctgcaaa ttaagacctt tgggtcaaggc 1560
 agcgggaatg cagccacgtt catcaacaac cacctcttga gcacgctagt gcttgaccag 1620
 tggaaacctg tgagacagcc cagaccagac agcgaggagt tcaaatcaat tgaggacaag 1680
 ctaggatatc actttaagat tgagaggtcc attgatgata tcaggggcaa gctgagacag 1740
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 ccaactgttg agcttgacct actagggttg tcagctacat acagcaaaga tctcgggatc 1860
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 gaggcgttga ggttggttag tggttggaac taccactcc tgaacaaagc ctgcaagaat 2040
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 gccgagtggc ctgagctgtc agagtccggg gaggccttcg aaggcttcaa tatcaagctg 2160
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 gtcaacagac cagtcaacac tgggggactc aaggcagtc gcaacgcct caagaccgtg 2280
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 gttcagtcga cttccgtgta cactcccaag taccagaag tcaagaacc acagaccgac 2580
 tccaaccccg ttgttgggct ccacctgccc gccaaagag ccaccgggtg ccaggccgct 2640

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cttctcggag caggaacgag cagaccaatg gggatggagg cccaacacg gtccaagaac 2700
gccgtgaaaa tggccaaacg gcggaacgc caaaaggaga gccgccaaca gccatgatgg 2760
gaaccactca agaagaggac actaatccca gaccccgat ccccgccctt cgcctgcggg 2820
ggcccc 2827

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<210> 76
<211> 2827
<212> DNA
<213> Infectious bursal disease virus

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<220>
<221> misc_feature
<222> (1)..(2827)
<223> cDNA sequence D6948-B of IBV B-segment

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<400> 76
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ccaccgctag ctgccacgtt agtggctcct cttcttgatg attctaccac catgagtgc 120
gttttcaata gtccacaggc gcgaagcaag atatcagcag cgttcggcat aaagcctaca 180
gctggacagg atgtggaaga actcctgatc cctaaggctt ggggtgccacc tgaggatccc 240
ttggccagcc ctatgcgtct ggccaagttc ctcagggaaa acggctacaa gattctgcag 300
ccacggtctc tacctgagaa tgaggagtat gagaccgatc aaatactccc tgacctagct 360
tggtatgaggc agatagaggg agctgtttta aaaccaaccc tatctctccc cattggagac 420
caggagtact tccctaaata ctaccaaca caccgcccga gcaaggaaaa gcccaatgcg 480
taccgccccg atctgcatt actcaagcag atgatctact tgtttctcca ggttcccag 540
gccacagata acctaaaga tgaggtcacc ctactaaccc aaaacattag agataaagcc 600
tacgggagtg ggacctacat gggacaggcc accagacttg ttgctatgaa agagggtgac 660
actgggagaa acccaaaca agatcctcta aagcttgggt acaccttga gagcatagcc 720
cagctacttg acatcacttt accggtaggc ccaccgggtg aggatgacaa gccctgggta 780
ccactcaciaa ggggtgccgtc aaggatggtg gttctgacgg gcgacgtaga tggggaattt 840
gaggttgagg actaccttcc caaatcaac ctcaagtcac caagtggact gccctatggt 900
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aggtacgaca aaagcactg gctaccaag accgtaaca tatggtcagc tccatcacca 1140
acacacctca tgatctcaat gataacctgg cccgtgatgt ccaatagccc aaacaacgtg 1200
ttgaacattg aggggtgtcc gtcactctac aagttcaacc cgttttagagg tgggctaaac 1260
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ctagttgtgg actcatcatg tctgattatg aaccttcaga tcaagacata tgggtcaaggc 1560
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aatgcaagtg cagctcggcg gcatctggag gccaaagggg tcccgtcga tgagttctc 2100
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gtcaacagac cagtcaacac cgggtgggcta aaggcagtc gcaatgccct caagaccggc 2280

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cggtatagaa atgaagccgg actaagtggc ctcgctcctcc tagccaccgc ccgcagccga 2340
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gaccccgatg cagactgggt tgaacgggtc gaaaccctgt cagacctgct ggagaaagcc 2460
gacattgcca gcaaggtcgc tcaactcagca ctcgtagaaa caagcgacgc tcttgaagcg 2520
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tccaaccccg ttgttgggct ccacctgccc gccaaaggag ccaccggtgt ccaggcagct 2640
cttctcggag cagggacgag cagaccaatg gggatggagg ctccaacacg gtccaagaac 2700
gccgtgaaaa tggccaaaag gcggcaacgc caaaaagaga gccgccaata gccatgatgg 2760
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ggcccc
2827

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<210> 77
<211> 1012
<212> PRT
<213> Infectious bursal disease virus

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<220>
<221> DOMAIN
<222> (1)..(1012)
<223> Consensus sequence of IBV polyprotein, whereby the Xaa
indicator may be any amino acid

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<220>
<221> MISC FEATURE
<222> (222)
<223> The 'Xaa' at position 222 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (253)
<223> The 'Xaa' at position 253 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (256)
<223> The 'Xaa' at position 256 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (279)
<223> The 'Xaa' at position 279 may be any amino acid

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<220>
<221> MISC FEATURE
<222> (284)
<223> The 'Xaa' at position 284 may be any amino acid

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<220>

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<221> MISC FEATURE
<222> (290)
<223> The 'Xaa' at position 290 may be any amino acid

<220>
<221> MISC FEATURE
<222> (294)
<223> The 'Xaa' at position 294 may be any amino acid

<220>
<221> MISC FEATURE
<222> (299)
<223> The 'Xaa' at position 299 may be any amino acid

<220>
<221> MISC FEATURE
<222> (330)
<223> The 'Xaa' at position 330 may be any amino acid

<220>
<221> MISC FEATURE
<222> (451)
<223> The 'Xaa' at position 451 may be any amino acid

<220>
<221> MISC FEATURE
<222> (541)
<223> The 'Xaa' at position 541 may be any amino acid

<220>
<221> MISC FEATURE
<222> (680)
<223> The 'Xaa' at position 680 may be any amino acid

<220>
<221> MISC FEATURE
<222> (685)
<223> The 'Xaa' at position 685 may be any amino acid

<220>
<221> MISC FEATURE
<222> (715)
<223> The 'Xaa' at position 715 may be any amino acid

<400> 77
Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
1 5 10 15
Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
20 25 30
Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
35 40 45
Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro

50		55		60
Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr				
65		70		75
Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr				
	85		90	95
Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr				
	100		105	110
Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr				
	115		120	125
Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu				
	130		135	140
Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val				
145		150		155
Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly				
	165		170	175
Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys				
	180		185	190
Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile				
	195		200	205
Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Xaa Gly Gly				
	210		215	220
Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu				
225		230		235
Ser Xaa Gly Gly Glu Leu Val Phe Gln Thr Ser Val Xaa Gly Leu Xaa				
	245		250	255
Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile				
	260		265	270
Thr Arg Ala Val Ala Ala Xaa Asn Gly Leu Thr Xaa Gly Thr Asp Asn				
	275		280	285
Leu Xaa Pro Phe Asn Xaa Val Ile Pro Thr Xaa Glu Ile Thr Gln Pro				
	290		295	300
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln				
305		310		315
Ala Gly Asp Gln Met Ser Trp Ser Ala Xaa Gly Ser Leu Ala Val Thr				
	325		330	335
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val				
	340		345	350

Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430
 Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Xaa Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Xaa Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640

Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Xaa Gly Glu Ile Glu Xaa Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Xaa Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr
 725 730 735
 Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln Tyr His Leu
 740 745 750
 Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala
 755 760 765
 Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser
 770 775 780
 Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp
 785 790 795 800
 Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn
 805 810 815
 Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu

930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

<210> 78
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein CEF94-PP

<400> 78
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15
 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30
 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45
 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60
 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80
 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
 85 90 95
 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110
 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
 115 120 125
 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160
 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175
 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190
 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205
 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly
 210 215 220
 Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
 225 230 235 240
 Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val
 245 250 255
 Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
 260 265 270
 Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn
 275 280 285
 Leu Leu Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro
 290 295 300
 Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
 305 310 315 320
 Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr
 325 330 335
 Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
 340 345 350
 Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
 355 360 365
 Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 370 375 380
 Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
 385 390 395 400
 Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
 405 410 415
 Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
 420 425 430

Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
 435 440 445
 Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
 450 455 460
 Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
 465 470 475 480
 Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
 485 490 495
 Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
 500 505 510
 Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
 515 520 525
 Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 530 535 540
 Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
 545 550 555 560
 Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
 565 570 575
 Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
 580 585 590
 Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly His Arg Val
 595 600 605
 Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr Gly Arg Asp
 610 615 620
 Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser Ile Met Leu
 625 630 635 640
 Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly Asn Leu Ala
 645 650 655
 Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile His Val Ala
 660 665 670
 Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys Val Ser Phe
 675 680 685
 Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu Lys Leu Ala
 690 695 700
 Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp Ala Thr Phe
 705 710 715 720
 Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr

<210> 79
 <211> 1012
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(1012)
 <223> Sequence of IBDV polyprotein D6948-PP

 <400> 79
 Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1 5 10 15

 Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
 20 25 30

 Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
 35 40 45

 Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
 50 55 60

 Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Ser Asn Gly Asn Tyr
 65 70 75 80

 Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
 85 90 95

 Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
 100 105 110

 Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
 115 120 125

 Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
 130 135 140

 Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
 145 150 155 160

 Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
 165 170 175

 Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
 180 185 190

 Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
 195 200 205

 Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Ala Gly Gly
 210 215 220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
225 230 235 240
Ser Ile Gly Gly Glu Leu Val Phe Gln Thr Ser Val Gln Gly Leu Ile
245 250 255
Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Ala Val Ile
260 265 270
Thr Arg Ala Val Ala Ala Asp Asn Gly Leu Thr Ala Gly Thr Asp Asn
275 280 285
Leu Met Pro Phe Asn Ile Val Ile Pro Thr Ser Glu Ile Thr Gln Pro
290 295 300
Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
305 310 315 320
Ala Gly Asp Gln Met Ser Trp Ser Ala Ser Gly Ser Leu Ala Val Thr
325 330 335
Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
340 345 350
Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
355 360 365
Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
370 375 380
Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
385 390 395 400
Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
405 410 415
Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
420 425 430
Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
435 440 445
Arg Ala Leu Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
450 455 460
Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
465 470 475 480
Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
485 490 495
Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
500 505 510
Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln

515					520					525					
Asn	Pro	Val	Val	Asp	Gly	Ile	Leu	Ala	Ser	Pro	Gly	Ile	Leu	Arg	Gly
530						535					540				
Ala	His	Asn	Leu	Asp	Cys	Val	Leu	Arg	Glu	Gly	Ala	Thr	Leu	Phe	Pro
545					550					555					560
Val	Val	Ile	Thr	Thr	Val	Glu	Asp	Ala	Met	Thr	Pro	Lys	Ala	Leu	Asn
				565					570					575	
Ser	Lys	Met	Phe	Ala	Val	Ile	Glu	Gly	Val	Arg	Glu	Asp	Leu	Gln	Pro
			580					585					590		
Pro	Ser	Gln	Arg	Gly	Ser	Phe	Ile	Arg	Thr	Leu	Ser	Gly	His	Arg	Val
		595					600					605			
Tyr	Gly	Tyr	Ala	Pro	Asp	Gly	Val	Leu	Pro	Leu	Glu	Thr	Gly	Arg	Asp
610						615					620				
Tyr	Thr	Val	Val	Pro	Ile	Asp	Asp	Val	Trp	Asp	Asp	Ser	Ile	Met	Leu
625					630					635					640
Ser	Lys	Asp	Pro	Ile	Pro	Pro	Ile	Val	Gly	Asn	Ser	Gly	Asn	Leu	Ala
				645					650					655	
Ile	Ala	Tyr	Met	Asp	Val	Phe	Arg	Pro	Lys	Val	Pro	Ile	His	Val	Ala
			660					665					670		
Met	Thr	Gly	Ala	Leu	Asn	Ala	Tyr	Gly	Glu	Ile	Glu	Asn	Val	Ser	Phe
		675					680					685			
Arg	Ser	Thr	Lys	Leu	Ala	Thr	Ala	His	Arg	Leu	Gly	Leu	Lys	Leu	Ala
						695					700				
Gly	Pro	Gly	Ala	Phe	Asp	Val	Asn	Thr	Gly	Ser	Asn	Trp	Ala	Thr	Phe
705					710					715					720
Ile	Lys	Arg	Phe	Pro	His	Asn	Pro	Arg	Asp	Trp	Asp	Arg	Leu	Pro	Tyr
				725					730					735	
Leu	Asn	Leu	Pro	Tyr	Leu	Pro	Pro	Asn	Ala	Gly	Arg	Gln	Tyr	Asp	Leu
			740					745					750		
Ala	Met	Ala	Ala	Ser	Glu	Phe	Lys	Glu	Thr	Pro	Glu	Leu	Glu	Ser	Ala
		755					760					765			
Val	Arg	Ala	Met	Glu	Ala	Ala	Ala	Asn	Val	Asp	Pro	Leu	Phe	Gln	Ser
	770					775					780				
Ala	Leu	Ser	Val	Phe	Met	Trp	Leu	Glu	Glu	Asn	Gly	Ile	Val	Thr	Asp
785					790					795					800
Met	Ala	Asn	Phe	Ala	Leu	Ser	Asp	Pro	Asn	Ala	His	Arg	Met	Arg	Asn
				805					810					815	

Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys
 820 825 830
 Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu
 835 840 845
 Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
 850 855 860
 Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
 865 870 875 880
 Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
 885 890 895
 Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
 900 905 910
 Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
 915 920 925
 Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
 930 935 940
 Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
 945 950 955 960
 Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
 965 970 975
 Pro Arg Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
 980 985 990
 Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Ala Val Ser Asp
 995 1000 1005
 Glu Asp Leu Glu
 1010

<210> 80
 <211> 290
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(290)
 <223> Sequence of IBDV polyprotein TY89-PP

<400> 80
 Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg Leu Pro Tyr Leu Asn
 1 5 10 15

Leu Pro Tyr Leu Pro Pro Thr Ala Gly Arg Gln Phe His Leu Ala Leu
 20 25 30
 Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Asp Ala Val Arg
 35 40 45
 Ala Met Asp Ala Ala Ala Asn Val Asp Pro Leu Phe Arg Ser Ala Leu
 50 55 60
 Gln Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala
 65 70 75 80
 Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Lys Asn Phe Leu
 85 90 95
 Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly
 100 105 110
 Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala
 115 120 125
 Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly
 130 135 140
 Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly
 145 150 155 160
 Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu Ile Pro
 165 170 175
 Glu Pro Asn Glu Asp Tyr Pro Asp Tyr Val His Ala Glu Lys Ser Arg
 180 185 190
 Leu Ala Ser Glu Glu Gln Val Leu Arg Ala Ala Thr Ser Ile Tyr Gly
 195 200 205
 Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala
 210 215 220
 Arg Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met
 225 230 235 240
 Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg
 245 250 255
 Arg Ala Pro Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Ser Gln Arg
 260 265 270
 Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp
 275 280 285
 Leu Glu
 290

<210> 81
 <211> 881
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(881)
 <223> Consensus sequence of IBDV VP1, ~~whereby the Xaa~~
~~indicator may be any amino acid~~

<220>
<221> MISC FEATURE
<222> (4)
<223> The 'Xaa' at position 4 may be any amino acid

<220>
<221> MISC FEATURE
<222> (13)
<223> The 'Xaa' at position 13 may be any amino acid

<220>
<221> MISC FEATURE
<222> (61)
<223> The 'Xaa' at position 61 may be any amino acid

<220>
<221> MISC FEATURE
<222> (145). . . (147)
<223> The 'Xaa' at positions 145-147 may be any amino acid

<220>
<221> MISC FEATURE
<222> (242)
<223> The 'Xaa' at position 242 may be any amino acid

<220>
<221> MISC FEATURE
<222> (287)
<223> The 'Xaa' at position 287 may be any amino acid

<220>
<221> MISC FEATURE
<222> (390)
<223> The 'Xaa' at position 390 may be any amino acid

<220>
<221> MISC FEATURE
<222> (393)
<223> The 'Xaa' at position 393 may be any amino acid

<220>
<221> MISC FEATURE
<222> (508)

<223> The 'Xaa' at position 508 may be any amino acid

<220>

<221> MISC FEATURE

<222> (511)

<223> The 'Xaa' at position 511 may be any amino acid

<220>

<221> MISC FEATURE

<222> (546)

<223> The 'Xaa' at position 546 may be any amino acid

<220>

<221> MISC FEATURE

<222> (562)

<223> The 'Xaa' at position 562 may be any amino acid

<220>

<221> MISC FEATURE

<222> (646)

<223> The 'Xaa' at position 646 may be any amino acid

<220>

<221> MISC FEATURE

<222> (687)

<223> The 'Xaa' at position 687 may be any amino acid

<220>

<221> MISC FEATURE

<222> (695)

<223> The 'Xaa' at position 695 may be any amino acid

<220>

<221> MISC FEATURE

<222> (880) . . . (881)

<223> The 'Xaa' at positions 880-881 may be any amino acid

<400> 81

Met Ser Asp Xaa Phe Asn Ser Pro Gln Ala Arg Ser Xaa Ile Ser Ala
1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
20 25 30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
35 40 45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Xaa Leu Gln Pro
50 55 60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
65 70 75 80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
85 90 95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140
 Xaa Xaa Xaa Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
 165 170 175
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240
 Gly Xaa Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Xaa Leu
 275 280 285
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
 305 310 315 320
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
 325 330 335
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380

Ile Val Glu Trp Ile Xaa Ala Pro Xaa Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
 485 490 495
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Xaa Gln Pro Xaa Pro
 500 505 510
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525
 Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540
 Val Xaa Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560
 Gln Xaa Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Xaa Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Xaa Glu

675	680	685
Ser Leu Ala Glu Leu Asn Xaa Pro Val Pro Pro Lys Pro Pro Asn Val		
690	695	700
Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu		
705	710	715
Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu		
	725	730
		735
Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala		
	740	745
		750
Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp		
	755	760
		765
Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp		
	770	775
		780
Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala		
785	790	795
		800
Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu		
	805	810
		815
Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu		
	820	825
		830
Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly		
	835	840
		845
Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala		
	850	855
		860
Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Xaa		
865	870	875
		880

Xaa

<210> 82
 <211> 881
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(881)
 <223> Sequence of IBDV CEF94-VP1

<400> 82
 Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
 1 5 10 15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30
 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
 35 40 45
 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
 50 55 60
 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80
 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95
 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110
 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125
 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140
 Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160
 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
 165 170 175
 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190
 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205
 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220
 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240
 Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu
 275 280 285
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro

305					310						315				320
Lys	Ala	Glu	Arg	Tyr	Asp	Lys	Ser	Thr	Trp	Leu	Thr	Lys	Thr	Arg	Asn
				325					330					335	
Ile	Trp	Ser	Ala	Pro	Ser	Pro	Thr	His	Leu	Met	Ile	Ser	Met	Ile	Thr
			340					345					350		
Trp	Pro	Val	Met	Ser	Asn	Ser	Pro	Asn	Asn	Val	Leu	Asn	Ile	Glu	Gly
		355					360					365			
Cys	Pro	Ser	Leu	Tyr	Lys	Phe	Asn	Pro	Phe	Arg	Gly	Gly	Leu	Asn	Arg
	370					375					380				
Ile	Val	Glu	Trp	Ile	Leu	Ala	Pro	Glu	Glu	Pro	Lys	Ala	Leu	Val	Tyr
385					390					395					400
Ala	Asp	Asn	Ile	Tyr	Ile	Val	His	Ser	Asn	Thr	Trp	Tyr	Ser	Ile	Asp
				405					410					415	
Leu	Glu	Lys	Gly	Glu	Ala	Asn	Cys	Thr	Arg	Gln	His	Met	Gln	Ala	Ala
			420					425					430		
Met	Tyr	Tyr	Ile	Leu	Thr	Arg	Gly	Trp	Ser	Asp	Asn	Gly	Asp	Pro	Met
		435					440					445			
Phe	Asn	Gln	Thr	Trp	Ala	Thr	Phe	Ala	Met	Asn	Ile	Ala	Pro	Ala	Leu
	450					455					460				
Val	Val	Asp	Ser	Ser	Cys	Leu	Ile	Met	Asn	Leu	Gln	Ile	Lys	Thr	Tyr
465					470					475					480
Gly	Gln	Gly	Ser	Gly	Asn	Ala	Ala	Thr	Phe	Ile	Asn	Asn	His	Leu	Leu
				485					490					495	
Ser	Thr	Leu	Val	Leu	Asp	Gln	Trp	Asn	Leu	Met	Arg	Gln	Pro	Arg	Pro
			500					505					510		
Asp	Ser	Glu	Glu	Phe	Lys	Ser	Ile	Glu	Asp	Lys	Leu	Gly	Ile	Asn	Phe
		515					520					525			
Lys	Ile	Glu	Arg	Ser	Ile	Asp	Asp	Ile	Arg	Gly	Lys	Leu	Arg	Gln	Leu
	530					535					540				
Val	Leu	Leu	Ala	Gln	Pro	Gly	Tyr	Leu	Ser	Gly	Gly	Val	Glu	Pro	Glu
545					550					555					560
Gln	Ser	Ser	Pro	Thr	Val	Glu	Leu	Asp	Leu	Leu	Gly	Trp	Ser	Ala	Thr
				565					570					575	
Tyr	Ser	Lys	Asp	Leu	Gly	Ile	Tyr	Val	Pro	Val	Leu	Asp	Lys	Glu	Arg
			580					585					590		
Leu	Phe	Cys	Ser	Ala	Ala	Tyr	Pro	Lys	Gly	Val	Glu	Asn	Lys	Ser	Leu
		595					600					605			

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
 820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln Gln
 865 870 875 880
 Pro

<210> 83
 <211> 879
 <212> PRT
 <213> Infectious bursal disease virus

 <220>
 <221> DOMAIN
 <222> (1)..(879)
 <223> Sequence of IBDV D6948-VP1

 <400> 83
 Met Ser Asp Val Phe Asn Ser Pro Gln Ala Arg Ser Lys Ile Ser Ala
 1 5 10 15

 Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
 20 25 30

 Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
 35 40 45

 Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Ile Leu Gln Pro
 50 55 60

 Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65 70 75 80

 Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
 85 90 95

 Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
 100 105 110

 Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
 115 120 125

 Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
 130 135 140

 Thr Asp Asn Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145 150 155 160

 Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu
 165 170 175

 Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
 180 185 190

 Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
 195 200 205

 Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
 210 215 220

 Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225 230 235 240

Gly Glu Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
 245 250 255
 Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
 260 265 270
 Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Ala Leu
 275 280 285
 Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
 290 295 300
 Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
 305 310 315 320
 Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
 325 330 335
 Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
 340 345 350
 Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
 355 360 365
 Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
 370 375 380
 Ile Val Glu Trp Ile Met Ala Pro Asp Glu Pro Lys Ala Leu Val Tyr
 385 390 395 400
 Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
 405 410 415
 Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
 420 425 430
 Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
 435 440 445
 Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
 450 455 460
 Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
 465 470 475 480
 Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
 485 490 495
 Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Lys Gln Pro Ser Pro
 500 505 510
 Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
 515 520 525

Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
 530 535 540
 Val Pro Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
 545 550 555 560
 Gln Pro Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
 565 570 575
 Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
 580 585 590
 Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
 595 600 605
 Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
 610 615 620
 Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
 625 630 635 640
 Cys Lys Asn Asn Ala Ser Ala Ala Arg Arg His Leu Glu Ala Lys Gly
 645 650 655
 Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
 660 665 670
 Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Pro Glu
 675 680 685
 Ser Leu Ala Glu Leu Asn Arg Pro Val Pro Pro Lys Pro Pro Asn Val
 690 695 700
 Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
 705 710 715 720
 Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
 725 730 735
 Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
 740 745 750
 Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
 755 760 765
 Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
 770 775 780
 Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 785 790 795 800
 Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
 805 810 815
 Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu

820 825 830
 Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
 835 840 845
 Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
 850 855 860
 Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg Gln
 865 870 875

<210> 84
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Consensus sequence of IBDV VP5, ~~whereby the Xaa~~
~~indicator may be any amino acid~~

<220>
<221> MISC FEATURE
<222> (14)
<223> The 'Xaa' at position 14 may be any amino acid

<220>
<221> MISC FEATURE
<222> (45)
<223> The 'Xaa' at position 45 may be any amino acid

<220>
<221> MISC FEATURE
<222> (74)
<223> The 'Xaa' at position 74 may be any amino acid

<220>
<221> MISC FEATURE
<222> (125)
<223> The 'Xaa' at position 125 may be any amino acid

<400> 84
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Xaa Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Xaa Glu Ala His
 35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 Val Arg Ala Asn Cys Leu Phe Pro Trp Xaa Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Xaa Trp Trp Arg
 115 120 125
 Leu Cys Thr Lys Xaa His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140
 Glu
 145

<210> 85
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBDV D6948-VP5

<400> 85
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Glu Pro Ala
 1 5 10 15
 Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30
 Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Arg Glu Ala His
 35 40 45
 Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60
 Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp Leu Asn Cys Gly
 65 70 75 80
 Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95
 Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
 100 105 110
 Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Pro Trp Trp Arg

115 120 125
 Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140

Glu
 145

<210> 86
 <211> 145
 <212> PRT
 <213> Infectious bursal disease virus

<220>
 <221> DOMAIN
 <222> (1)..(145)
 <223> Sequence of IBDV CEF94-VP5

<400> 86
 Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
 1 5 10 15

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
 20 25 30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
 35 40 45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
 50 55 60

Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
 65 70 75 80

Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln Val Arg Ser Asp
 85 90 95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Gln Ala
 100 105 110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
 115 120 125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
 130 135 140

Glu
 145

<210> 87
 <211> 149
 <212> PRT
 <213> Infectious bursal disease virus

<220>

<221> DOMAIN

<222> (1)..(149)

<223> Sequence of IBDV D6948-VP5

<400> 87

Met Leu Ser Leu Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp
1 5 10 15

Asp Glu Pro Ala Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu
20 25 30

Pro Ser Asp Ala Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro
35 40 45

Arg Glu Ala His Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys
50 55 60

Gly Gly His Arg Val Arg Ala Asn Cys Leu Phe Pro Trp Phe Pro Trp
65 70 75 80

Leu Asn Cys Gly Cys Ser Leu His Thr Ala Glu Gln Trp Glu Leu Gln
85 90 95

Val Arg Ser Asp Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln
100 105 110

Leu Leu Gln Ala Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr
115 120 125

Pro Trp Trp Arg Leu Cys Thr Lys Trp His His Lys Arg Arg Asp Leu
130 135 140

Pro Arg Lys Pro Glu [—————]
145